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RAW SEQUENCE LISTING

DATE: 05/24/2002

PATENT APPLICATION: US/10/032,366

TIME: 16:28:18

Input Set : N:\Crif3\RULE60\10032366.raw

Output Set: N:\CRF3\05242002\J032366.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Bandman, Olga
- 6 Guegler, Karl J.
- 7 Shah, Purvu
- 9 (ii) TITLE OF INVENTION: HUMAN RETINOID BINDING PROTEIN
- 11 (iii) NUMBER OF SEQUENCES: 4
- 13 (iv) CORRESPONDENCE ADDRESS:
- 14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
- 15 (B) STREET: 3174 Porter Drive
- 16 (C) CITY: Palo Alto
- 17 (D) STATE: CA
- 18 (E) COUNTRY: USA
- 19 (F) ZIP: 94304

ENTERED

21 (v) COMPUTER READABLE FORM:

- 22 (A) MEDIUM TYPE: Diskette
- 23 (B) COMPUTER: IBM Compatible
- 24 (C) OPERATING SYSTEM: DOS
- 25 (D) SOFTWARE: FastSEQ for Windows Version 2.0

27 (vi) CURRENT APPLICATION DATA:

- C--> 28 (A) APPLICATION NUMBER: US/10/032,366
- C--> 29 (B) FILING DATE: 21-Dec-2001
- 30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

- 33 (A) APPLICATION NUMBER: US/08/899,031
- 34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

- 37 (A) NAME: Billings, Lucy J.
- 38 (B) REGISTRATION NUMBER: 36,749
- 39 (C) REFERENCE/DOCKET NUMBER: PF-0349 US

41 (ix) TELECOMMUNICATION INFORMATION:

- 42 (A) TELEPHONE: 415-855-0555
- 43 (B) TELEFAX: 415-845-4166
- 44 (C) TELEX:

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 135 amino acids
- 51 (B) TYPE: amino acid
- 52 (C) STRANDEDNESS: single
- 53 (D) TOPOLOGY: linear

55 (vii) IMMEDIATE SOURCE:

- 56 (A) LIBRARY: SYNORAT01
- 57 (B) CLONE: 367304

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59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

61 Met Pro Pro Asn Leu Thr Gly Tyr Tyr Arg Phe Val Ser Gln Lys Asn
62 1 5 10 15
63 Met Glu Asp Tyr Leu Gln Ala Leu Asn Ile Ser Leu Ala Val Arg Lys
64 20 25 30
65 Thr Ala Leu Leu Lys Pro Asp Lys Glu Ile Glu His Gln Gly Asn
66 35 40 45
67 His Met Thr Val Arg Thr Leu Ser Thr Phe Arg Asn Tyr Thr Val Gln
68 50 55 60
69 Phe Asp Val Gly Val Glu Phe Glu Glu Asp Leu Arg Ser Val Asp Gly
70 65 70 75 80
71 Arg Lys Cys Gln Thr Ile Val Thr Trp Glu Glu Glu His Leu Val Cys
72 85 90 95
73 Val Gln Lys Gly Glu Val Pro Asn Arg Gly Trp Arg His Trp Leu Glu
74 100 105 110
75 Gly Glu Met Leu Tyr Leu Glu Leu Thr Ala Arg Asp Ala Val Cys Glu
76 115 120 125
77 Gln Val Phe Arg Lys Val Arg
78 130 135

```

80 (2) INFORMATION FOR SEQ ID NO: 2:

82 (i) SEQUENCE CHARACTERISTICS:

83 (A) LENGTH: 957 base pairs

84 (B) TYPE: nucleic acid

85 (C) STRANDEDNESS: single

86 (D) TOPOLOGY: linear

88 (vii) IMMEDIATE SOURCE:

89 (A) LIBRARY: SYNORAT01

90 (B) CLONE: 367304

92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

94 GTGTGGAGCT GGCTGGAATC TCTCAGCCTC ACCTGCCAGA CAACACCCCC TCCTTCCTCA 60
95 CCCTGTCTCC TGCATTCTCC TGAAACCTTC ATCCACACAA TGCCTCCCAA CCTCACTGGC 120
96 TACTACCGCT TTGTCTCGCA GAAGAACATG GAGGACTACC TGCAAGCCCT AAACATCAGC 180
97 TTGGCTGTGC GGAAGACCGC GCTGCTGCTG AAGCCGGACA AGGAGATCGA ACACCAGGGC 240
98 AACCACATGA CCGTGAGGAC GCTCAGCACC TTCCGAAACT AACTGTGCA GTTTGATGTG 300
99 GGAGTGGAGT TTGAGGAGGA CCTCAGGAGC GTGGACGGAC GAAAATGCCA GACCATAGTA 360
100 ACCTGGGAGG AGGAGCACCT GGTGTGTGTG CAGAAAGGGG AGGTCCCCAA CCGGGGCTGG 420
101 AGACACTGGC TGGAGGGAGA GATGCTGTAT CTGGAACCTGA CTGCAAGGGA TGCAGTGTGC 480
102 GAGCAGGTCT TCAGGAAGGT CAGATAGCCG GAGAGGAGCC AAGATCCCTC CAGACAGCAC 540
103 CAGCTCACAG ACGCTCTTGT TGTGCCCCCT TCAAGCCCAG ATTGTGCCAG GTCAGCTGTC 600
104 CTTTCCTCTG GCCACCTTTC CTCCCTCTGG GTCCCTCCTC ACCCCTCCCC GTGTTAATCT 660
105 GTAACCTTGA CCCCCAGGC CAAAGTCCTT TCTCAGCTC CACTGCCCAA TAGTGACCTC 720
106 ACTTCCAGGT CAAGGTCTGG CGTCCCAAAT GAAAGAAGCA GGCAAAGGGA AGGAGCCCCCT 780
107 GAGAACAACC AATCTCCGCT CTCTCCTGTC CATTTGACCT CTTCTTTTCC TTCTAAGAAA 840
108 GAACTAAGCT TTGGGCATTT GGCGATTAGT GAAATTTCTA TCCTGATGGA CTTCTGGAAA 900
109 ACTGTGACTG GGGTTCAAGA GTTTAAACAG GGGCTACTGG CAGAGANAAA AAAAAAAA 957

```

111 (2) INFORMATION FOR SEQ ID NO: 3:

113 (i) SEQUENCE CHARACTERISTICS:

114 (A) LENGTH: 135 amino acids

115 (B) TYPE: amino acid

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```

116          (C) STRANDEDNESS: single
117          (D) TOPOLOGY: linear
119      (vii) IMMEDIATE SOURCE:
120          (A) LIBRARY: GenBank
121          (B) CLONE: 50548
123      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
125  Met Pro Val Asp Phe Asn Gly Tyr Trp Lys Met Leu Ser Asn Glu Asn
126  1      5      10      15
127  Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys
128      20      25      30
129  Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp
130      35      40      45
131  His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp
132      50      55      60
133  Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp
134      65      70      75      80
135  Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
136      85      90      95
137  Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu
138      100     105     110
139  Gly Asp Glu Leu His Leu Glu Met Arg Ala Glu Gly Val Ile Cys Lys
140      115     120     125
141  Gln Val Phe Lys Lys Val His
142      130     135
144  (2) INFORMATION FOR SEQ ID NO: 4:
146      (i) SEQUENCE CHARACTERISTICS:
147          (A) LENGTH: 135 amino acids
148          (B) TYPE: amino acid
149          (C) STRANDEDNESS: single
150          (D) TOPOLOGY: linear
152      (vii) IMMEDIATE SOURCE:
153          (A) LIBRARY: GenBank
154          (B) CLONE: 190948
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
158  Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn
159  1      5      10      15
160  Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys
161      20      25      30
162  Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp
163      35      40      45
164  His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp
165      50      55      60
166  Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp
167      65      70      75      80
168  Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
169      85      90      95
170  Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu
171      100     105     110
172  Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys

```

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173		115		120		125	
174	Gln	Val	Phe	Lys	Lys	Val	Gln
175		130				135	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/032,366

DATE: 05/24/2002

TIME: 16:28:19

Input Set : N:\Crif3\RULE60\10032366.raw

Output Set: N:\CRF3\05242002\J032366.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]